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United States Department of the Interior

BUREAU of RECLAMATION
Central Valley Operations Office
3310 El Camino Avenue, Suite 300
Sacramento, California 95821

NOV 17 2017

IN REPLY
REFER TO

CV0-150
ENV-7.00

Ms. Maria Rea
Supervisor
Central Valley Office
National Marine Fisheries Service
650 Capitol Mall, Suite 5-100
Sacramento, CA 95814

Subject: Rapid Genetic Analysis of the Central Valley Project (CVP) and State Water Project (SWP) Salvaged Chinook Salmon in Water Year (WY) 2018

Dear Ms. Rea:

Please find enclosed a procedure for implementing rapid genetic analysis of CVP and SWP salvaged older juvenile Chinook salmon *(Oncorhynchus tshawytscha)*. This procedure was used as a pilot effort during the last two water years. It was described in letters to the National Marine Fisheries Service (NMFS) dated April 13, 2016, and October 20, 2016. In a letter dated May 6, 2016, NMFS agreed that the protocol for the rapid genetic analysis allowed for the identification of older juvenile Chinook salmon to race. Additionally, in a letter dated November 21, 2016, NMFS supported the use of this protocol for WY 2017, with the two additional conditions that all unclipped Chinook salmon have tissue samples collected for subsequent analysis, and that the annual incidental take limit was set at one percent of natural winter-run.

Rapid genetic analysis aids in determining an accurate estimation of loss at the CVP and SWP fish salvage facilities for the Sacramento River winter-run Chinook salmon, listed as endangered under the Endangered Species Act (ESA) of 1973, as amended (16 U.S.C. 1531 et seq.). Rapid genetic analysis allows for timely discrimination of different races of Chinook salmon. The different races of Chinook salmon may overlap within the older juvenile size-at-date criteria used at the fish salvage facilities, some of which are ESA-listed (winter-run Chinook salmon and Central Valley spring-run Chinook salmon) and some of which are non-listed races under the ESA (fall-run and late fall-run Chinook salmon).

The Bureau of Reclamation (Reclamation) plans to implement the same procedure during WY 2018. Reclamation and the Department of Water Resources (DWR), in consultation with the California Department of Fish and Wildlife (CDFW), U.S. Fish and Wildlife Service, and NMFS, previously developed this procedure to genetically identify ESA-listed fish species that fit within the older juvenile size-at-date criteria at the fish salvage facilities. The procedure describes a timeline for preliminary and final loss estimation based on updated genetic information, which may prove useful in achieving salmonid protection and water reliability during periods when ESA-listed species are present in the Sacramento-San Joaquin Delta.

The procedure will increase the accuracy of information utilized to implement Reasonable and Prudent Alternative (RPA) actions IV.2.3 and IV.3 in theNMFS 2009 Biological Opinion on the Coordinated Long-term Operation of the CVP and SWP. For WY 2018, Reclamation and DWR have contracts with the CDFW Central Valley Tissue Archive and Cramer Fish Sciences to carry out rapid archiving and genetic analysis of salvaged fish tissue. The genetic analysis will determine the run of each individual Chinook salmon from the tissue sent for analysis.

The procedure was based on a method used by NMFS for this purpose in WY 2015. However, the described procedure takes a more precautionary approach. Actions to reduce pumping at the CVP and SWP export facilities are executed once the older juvenile counts exceed the trigger threshold. If the salvaged older juveniles are genetically confirmed ESA-listed species, protective actions will continue. If the older juvenile Chinook salmon are not genetically an ESA-listed species and pumping reduction triggers are not met or exceeded, then export reductions will be rescinded.

Reclamation appreciates the assistance of members of the Delta Operation for Salmon and Sturgeon work team, who previously provided review of the enclosed procedure. Should you have any questions or concerns, please contact Mr. Mike Hendrick in our Bay Delta Office at 916-414-2420 or by email at mhendrick@usbr.gov.

Sincerely,

Jeff Rieker
Operations Manager

Enclosure

cc: Mr. John Leahigh
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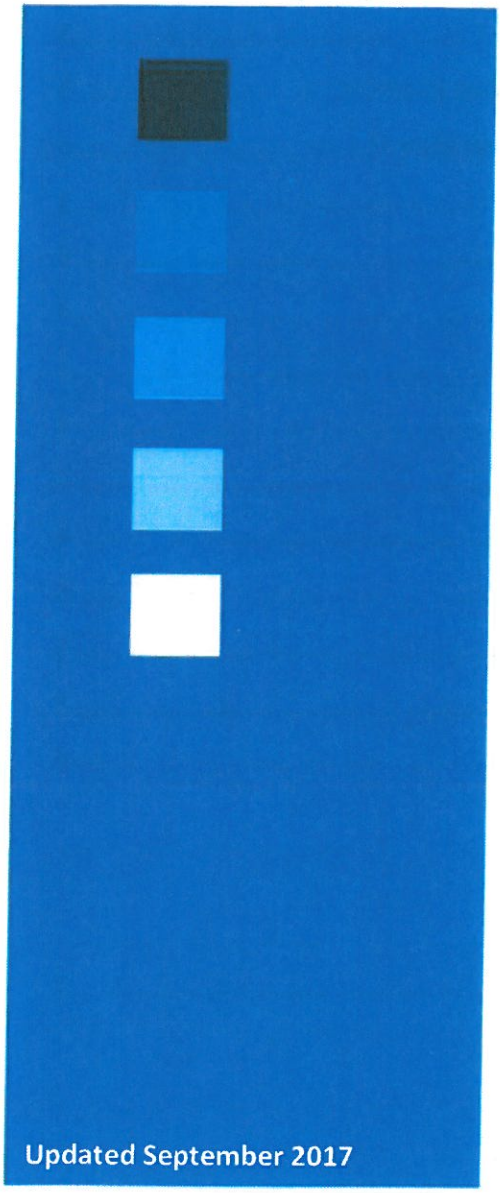
(w/encl to each)

PROCEDURES FOR RAPID ANALYSIS OF SALVAGED CHINOOK SALMON



Updated September 2017

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GENIDAQS℠

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1. Overview

This process of rapid genetic analysis of salvaged older juvenile Chinook Salmon is for November 2017 through June 2018. These "older juveniles" are at or above the minimum winter-run size based on the length-at-date model at the fish collection facilities and below the maximum size considered by the length-at-date model, on a given date. This period is inclusive of the duration of actions IV.2.1, IV.2.3, and IV.3 in the NMFS Biological Opinion on the Coordinated Long term Operations of the Central Valley Project and State Water Project.

All references to a specific day includes weekend days and holidays, unless noted otherwise.

2. Procedures

A. Salvage Data on Fax Sheet at Fish Facilities

1. Operations and Count Summary Data Sheet Previous 24 hours

a. Salvage data includes operational and count summary for 12:00am to 11:59pm of the previous day.
b. Salvage data sheets checked (for the previous day) and emailed by 9:00 am each day by fish collection facility staff.

B. Preliminary Reporting of Loss through Laboratory Arrival (Day 1)

1 Preliminary LOSS

a. This happens by 9:00 am
b. If fish are counted that meet size-at-date criterion for older juveniles and no loss density trigger or annual take limit is reached then DNA-based run assignment of fish will be determined later (accompanying the next set of rapidly analyzed samples). Under non-rapid analysis conditions the BOR contract manager may still request that the DNA-based run assignment be run anytime. This may be important if triggers are not being exceeded, a large number of samples are collected, and there is a desire for accurate genetic identification.
c. Preferably by 8:00a and by no later than 9:00a, CDFW's Central Valley Tissue Archive staff (CVTA) and Cramer Fish Sciences (CFS) staff will be notified by USBR staff as to whether or not rapid processing is needed for that day.
d. If preliminary loss calculations indicate a trigger is reached then:
    a. the preliminary loss calculation will be confirmed or corrected via a Quality Assurance/ Quality Control (QA/QC) process
        i. If trigger is on weekday then CDFW does QA/QC.
        ii. If trigger is on weekend then USBR does QA/QC.
e. CVP/SWP operational contacts are notified of trigger exceedance.
    a. Operational contacts notify NMFS and CDFW contacts.
    b. Operators automatically begin implementing RPA action response.

2. Receipt and Sample Transport

a. This is an approximately four hour process.
b. If rapid analysis needs to occur (see step B.1.c), CVTA staff will proceed to the facilities (CVP/SWP as needed) to retrieve samples (CVTA staff should retrieve all samples present).

c. CVTA will notify CVP/SWP facility staff that persons are on route to retrieve samples.
d. Chain of Custody (COC) will start at facilities
e. The CVTA staff checks all sample vials with the data sheets, making sure they match, the data are complete, and that the data makes sense (date/time in chronological order, data legible, etc.).
f. If the CVTA staff have notes about the sample (i.e., yellow EtOH, multiple samples in vial) they will write it down on the data sheet and initial it.
g. The CVTA staff will leave copies of the data sheets at the facility.
h. Tissues will be brought to the CVTA and CVTA will retain a portion of sample; and the other portion of sample will be prepared for transfer to CFS laboratory. CVTA staff will notify CFS staff when samples will be available for transfer.
i. At the direction of the USBR contract manager, CVTA will prepare additional pre-extracted staged samples for analysis to minimize empty wells on the genotyping plate.

C. Sample Receiving and Analysis

1. Sample "log in"/receipt.

a. This is a less than one hour process.
b. Notify CFS staff when CVTA staff return from the pumps (including the number of samples picked up) so CFS staff can start heading over to pick up the split samples. If something unexpected occurs and sample delivery is delayed or will not occur, CFS, DWR and Reclamation will be notified as soon as possible.
c. CFS and CVTA will account for samples received. CFS will verify the COC ID's, sample tube ID's and contents.
d. CFS will generate a QA/QC report and communicate to the USBR contract manager.
e. A copy of COC and QA/QC will be emailed to USBR contract manager.

2. DNA extraction

a. This is a 3 hour process for up to 96 samples
b. Sample ID's will be entered into CFS database
c. DNA extraction will be done by automated laboratory robot.

3. Genotyping

a. This is a 5 hour process for up to 96 samples.
b. This step includes pre-amplification of samples, chip loading, and sample cycling. Poor sample quality may prevent the production of genotype information. If a verified sample pre-screening process is developed that is predictive of genotype failure, this procedural step will be included. Pre-screening will not guarantee results, which may be delayed or unavailable due to poor material quality.
c. This step will use positive and no template controls on the standard west coast salmonid 96-SNP panel.
d. This step will generate raw genotype and verification of positive control and no template controls.

4. Genetic Identification (Day 2)

a. Laboratory will review raw genotypes and undertake data processing (R code for processing).

b. Data will be used in Mixed Stock Analysis using ONCOR and NOAA reference database.
c. CFS will generate report including at least the following information:
    i. Sample number,
    ii. size-at-date identity of each sample,
    iii. genetic identity of each sample, and
    iv. assignment scores (i.e. maximum likelihood) to each baseline population
d. CFS will distribute to USBR Contracting Officer Representative and DWR Task Manager.

D. Genetically-identified LOSS

1. Results of genetically-identified LOSS estimate will be calculated by DWR (weekdays) or USBR (weekends) and sent to NMFS and DFW contacts.
2. Results will also be communicated to appropriate operations teams (DOSS, WOMT, other management team (TBD)).

E. Operational Decision

1. Operational decision will be reviewed:
    (a) If genetic-based run determination(s) matches size-at-date-based run determination(s), then no change in action is needed.
    (b) If genetic-based run determination(s) does *not* match size-at-date-based run determination(s), genetically-identified loss used for implementing appropriate action (i.e. rescind action, shift to lower exceedance action).

F. Documentation

1. Data records will be updated, as appropriate (CDFW salvage database).
2. Genetic assignment results and associated operational decisions will be reviewed at DOSS during the following week and captured in the DOSS notes.

3. WATER YEAR 2018 CONTACT LIST

CDFW Contact: Ken Kundargi

Central Valley Tissue Archive (CVTA) Staff: Lea Koerber

Cramer Fish Sciences Staff: Gregg Schumer

CVP Operation Contact: Jeff Rieker

DWR Task Manager (CVTA contract): Kevin Reece

NMFS contact: Garwin Yip

Reclamation Contracting Officer Representative (genetic identification contract): Josh Israel

SWP Operation Contact: John Leahigh

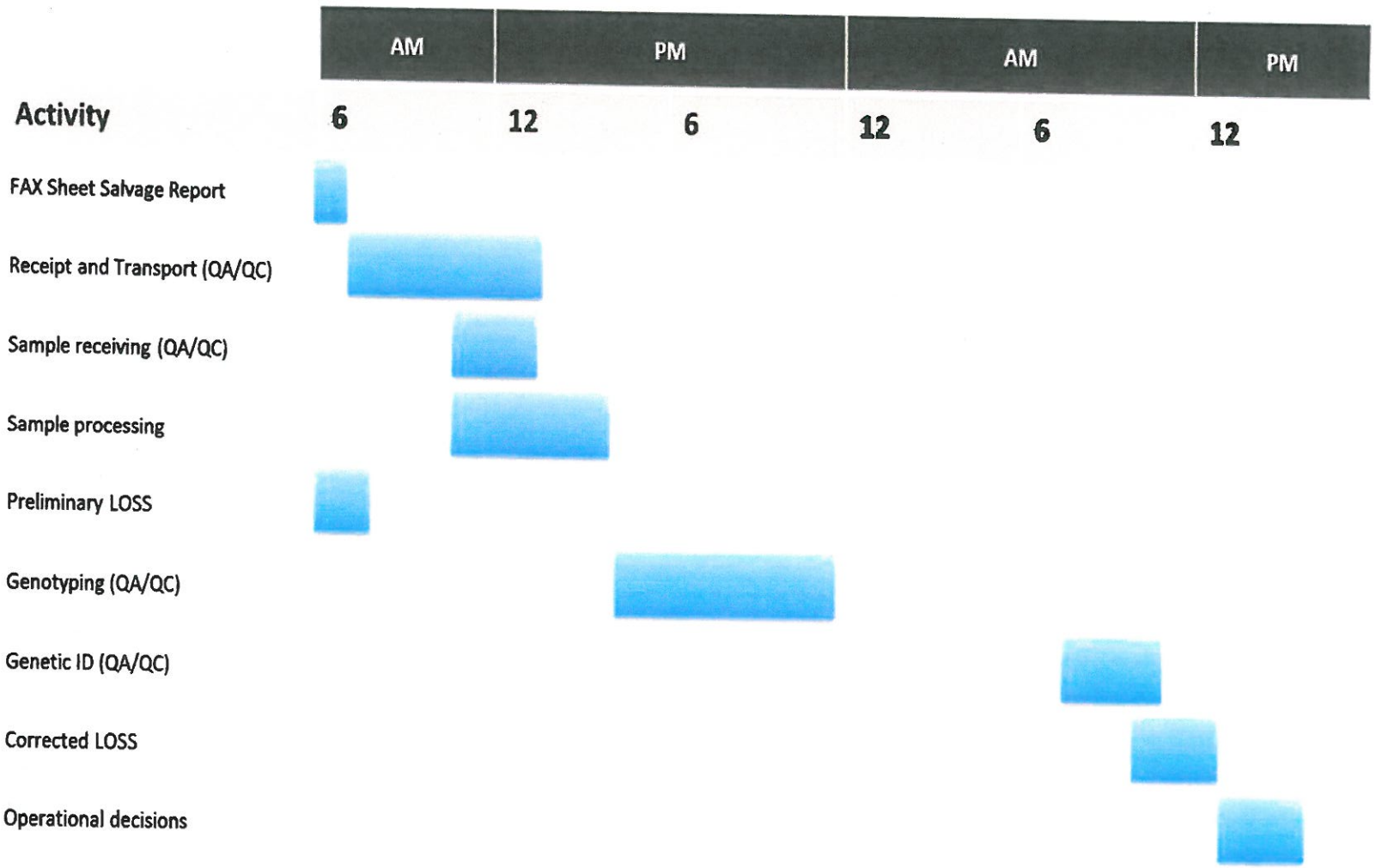

Figure 1. Gantt chart for rapid salvage ID process